



Genomic Epidemiology

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Genomic Epidemiology

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WGS holds the promise to revolutionize surveillance and diagnostics of infectious diseases due to its high resolution. It may be used across many areas such as monitoring food, environment, clinical, veterinary, wildlife, etc., for all known pathogens, i.e., viruses, bacteria, fungi, parasites, etc. A major obstacle is how to create a robust and simple to use system that will allow its adaptation within the relevant labs. A goal would be to establish a Web-based system, allowing users to upload sequence and meta data for several isolates in one batch upload, and have several analysis made on each isolate: assembly, species typing, MLST typing (for bacteria), resistance gene finding, virulence prediction, and gene finding. Furthermore the system should allow single nucleotide polymorphism (SNP) based comparison of the uploaded isolates with all previously uploaded isolates.

The Center for Genomic Epidemiology (CGE) has, over the last 4 years, worked on developing a system for surveillance and diagnostics of infectious diseases. This system has been running since 2012 (genomicepidemiology.org). So far, more than 150,000 isolates have been analyzed. This has demonstrated that online analysis of WGS information is possible. This means it should be possible to create a unified portal so that all area and pathogen data can be compared, enabling us to trace back all infections. The work will in the coming years be continued in the context of the COMPARE project.